

■ Incorporating an immune response

The Basic Model does not account for immune processes (such as CD8+ cytotoxic T lymphocytes) controlling viral load by encountering HIV-1 infected cells and killing them. Immune recognition occurs because HIV-1 proteins and protein fragments are presented on the membrane of infected cells.

Here we incorporate an immune response into the crHIV-1 model.

Immune cells (Z) kill HIV-1 productively infected cells at a per cell rate κ and kill productive I_D cells at per cell rate κ' . Immune cells also die at a rate δ_Z .

Cells infected only with crHIV-1 are not recognized by immune cells because they do not express HIV-1 proteins that can be presented on the cell membrane.

$$\begin{aligned}
 \dot{T} &= \lambda - dT - kVT - kV_T T \\
 \dot{I}_1 &= kVT - bI_1 \\
 \dot{I}_2 &= b(I_1 - I_2) \\
 &\dots \\
 \dot{I}_m &= bI_{m-1} - \delta_0 I_m - \kappa Z I_m \\
 \dot{I}_T &= kTV_T - dI_T - kVI_T \\
 \dot{I}_{D_1} &= kVT - bI_{D_1} \\
 \dot{I}_{D_2} &= b(I_{D_1} - I_{D_2}) \\
 &\dots \\
 \dot{I}_{D_m} &= bI_{D_{m-1}} - \delta_0' I_{D_m} - \kappa' Z I_{D_m} \\
 \dot{V} &= n\delta I_m + Dn\delta' I_{D_m} - cV \\
 \dot{V}_T &= P^2 Dn\delta' I_{D_m} - cV_T
 \end{aligned}$$

for completeness we tried a variety of functions to describe how Z cells are activated (α)

$$\begin{aligned}
 \dot{Z} &= \alpha I_m - \delta_Z Z \\
 \text{or} \\
 \dot{Z} &= \alpha (I_m + I_{D_m}) - \delta_Z Z \\
 \text{or} \\
 \dot{Z} &= \alpha Z (I_m + I_{D_m}) - \delta_Z Z \\
 \text{or}
 \end{aligned}$$

$$\dot{Z} = \alpha - \delta_Z Z$$

(as above we used $b = 16$, $m = 30$, α and κ were calculated so that steady state was the initial condition for the simulations)

None of these models affect the qualitative behavior of the crHIV-1 gene therapy model because crHIV-1 converts the susceptible cell population T into a different reservoir of crHIV-1 transduced cells. Thus, the crHIV-1 effect on HIV-1 can be roughly mimicked by decreasing λ or increasing d in the Basic Model.